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# **Title: Free fatty acid binding pocket in the locked structure of SARS-CoV-2 spike protein**

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**Abstract:**

COVID-19, caused by severe acute respiratory syndrome-coronavirus-2 (SARS-CoV-2), represents a global crisis. Key to SARS-CoV-2 therapeutic development is unraveling the mechanisms driving high infectivity, broad tissue tropism and severe pathology. Our 2.85Å cryo-EM structure of SARS-CoV-2 spike (S) glycoprotein reveals that the receptor binding domains (RBDs) tightly bind the essential free fatty acid (FFA) linoleic acid (LA) in three composite binding pockets. The pocket also appears to be present in the highly pathogenic coronaviruses SARS-CoV and MERS-CoV. LA binding stabilizes a locked S conformation giving rise to reduced ACE2 interaction *in vitro*. In human cells, LA supplementation synergizes with the COVID-19 drug remdesivir, suppressing SARS-CoV-2 replication. Our structure directly links LA and S, setting the stage for intervention strategies targeting LA binding by SARS-CoV-2.

**One Sentence Summary:**

The SARS-CoV-2 spike binds linoleic acid, a key molecule in inflammation, immune modulation and membrane fluidity.

## Main Text:

Seven coronaviruses are known to infect humans. The four endemic human coronaviruses OC43, 229E, HKU1 and NL63 cause mild upper respiratory tract infections while pandemic virus SARS-CoV-2, and earlier SARS-CoV and MERS-CoV, can cause severe pneumonia with acute respiratory distress syndrome, multi-organ failure, and death (1,2).

SARS-CoV-2 has acquired functions that promote its harsh disease phenotype. SARS-CoV-2 causes severe inflammation and damage to endothelial cells in the heart, kidneys, liver and intestines, suggestive of a vascular infection rather than a purely respiratory disease (3, 4). The attachment of SARS-CoV-2 to a host cell is initiated by the spike protein trimer (S), which decorates the outer surface of the virus, binding to its cognate receptor angiotensin-converting enzyme 2 (ACE2), with higher affinity than SARS-CoV (5-7). A S1/S2 polybasic furin protease cleavage site distinguishes SARS-CoV-2 from SARS-CoV or other closely related bat coronaviruses and serves to stimulate entry into host cells and cell-cell fusion (5, 8, 9). Inside the host cell, human coronaviruses remodel the lipid metabolism to facilitate virus replication (10). Infection by SARS-CoV-2 triggers an unusually impaired and dysregulated immune response (11) and a heightened inflammatory response (12) working in synergy with interferon production in the vicinity of infected cells to drive a feed-forward loop to upregulate ACE2 and further escalate infection (13).

In the search for additional functions that contribute to the pathology of infection, we determined the structure of the SARS-CoV-2 S glycoprotein by cryo-EM (Fig. 1). We produced SARS-CoV-2 S as a secreted trimer (14) in MultiBac (15) baculovirus-infected Hi5 insect cells (fig. S1, (16)). Highly purified protein was used for cryo-EM data collection (fig. S2, table S1). After 3D classification and refinement without applying symmetry (C1) we obtained a 3.0 Å closed

conformation from 136,405 particles and a 3.5 Å open conformation with one receptor-binding domain (RBD) in the up position from 57,990 particles (figs. S2, S3). C3 symmetry was applied to the closed conformation particle pool yielding a 2.85 Å map (Fig.1A, figs. S2, S3).

The structure of S displays the characteristic overall shape observed for coronavirus S proteins in the closed and open conformations (17-19) with the closed form (~70%) predominating in our data set (Fig.1A, figs. S2-S4). Model building of the closed form revealed additional density in the RBDs in our structure (Fig.1B). The tube-like shape of this density was consistent with a fatty acid, with size and shape similar to LA bound to other proteins (Fig.1B, fig. S5) (20, 21). Liquid chromatography coupled ESI-TOF mass spectrometry (LS-MS) analysis confirmed the presence of a compound with the molecular weight of LA in our purified sample (Fig.1C).

Hallmarks of FFA-binding pockets in proteins are an extended 'greasy' tube lined by hydrophobic amino acids which accommodates the hydrocarbon tail, and a hydrophilic, often positively charged anchor for the acidic headgroup of the FFA. In our structure, a hydrophobic pocket mostly shaped by phenylalanines forms a bent tube into which the LA fits well (Fig. 1D,E). The anchor for the headgroup carboxyl is provided by an arginine (R408) and a glutamine (Q409) from the adjacent RBD in the trimer, giving rise to a composite LA-binding site (Fig. 1E). We confirmed the presence of LA in all three binding pockets in the S trimer in the unsymmetrized (C1) closed structure (fig. S6). Similarly, masked 3D classification focusing on the RBD domains could not identify any unoccupied pockets (fig. S7).

Our S construct contains alterations as compared to native SARS-CoV-2 S namely addition of a trimerization domain and deletion of the polybasic cleavage site, neither of which alter S conformation appreciably (14, 17) (fig. S8). Glycosylation sites are located away from the LA-binding pocket and largely native in our structure (7, 17) (table S2). Thus, neither mutations nor

glycosylation are likely to impact the LA-binding pocket. We compared S and RBD produced in insect cells with mammalian produced S to identify any potential influence of differences in glycosylation on ACE2 binding by competition enzyme-linked immunosorbent assay (ELISA) (Fig. 2A). All three reagents bound ACE2 efficiently. We further confirmed ACE2 binding by S using SEC with purified proteins (Fig. 2B). The LA-binding pocket and the receptor binding motif (RBM) are distal and non-overlapping (Fig. 2C). Notably, in the LA-bound S the RBM is ordered and buried at the interface between RBDs while it was disordered in previously described SARS-CoV-2 S cryo-EM structures (7, 17).

SARS-CoV-2 S can also adopt an open conformation (fig. S4) which is compatible with binding ACE2. In previous apo S cryo-EM structures about 60-75% of the S trimers were in the open conformation (7, 17), contrasting our observation of ~70% in the closed conformation. This could be due to LA stabilizing the closed conformation, and if so LA would be expected to reduce ACE2 binding. We performed surface plasmon resonance (SPR) experiments with biotinylated ACE2 immobilized on a streptavidin-coated chip (Fig. 2D, fig. S9). We first determined the  $K_D$  of the RBD / ACE2 interaction to validate our assay. Our value (26 nM, fig. S9C) is in good agreement with previous studies (44 nM, (22)) obtained by SPR with the RBD immobilized and ACE2 as analyte. Apo S was prepared by applying Lipidex, the established method for removing lipids from lipid-binding proteins (23). A  $K_D$  of 0.7 nM was obtained for the apo S / ACE2 interaction (fig. S9A). For the LA-bound S / ACE2 interaction we obtained a  $K_D$  of 1.4 nM (fig. S9B). We consistently obtained a markedly reduced resonance unit (RU) signal for LA-bound S as compared to apo S at the same concentrations (Fig. 2D, fig. S9A,B). This correlates with the apo state having a higher percentage of S trimers in the open, ACE2-accessible conformation.

We characterized the affinity of the LA interaction both experimentally and computationally. Our SPR assays utilizing immobilized RBD yielded a binding constant of ~41 nM exhibiting a slow off-rate, consistent with tight binding of LA (fig. S10). Repeated molecular dynamics simulations of the entire locked LA-bound spike trimer (3 x 100 ns) using GROMACS-2019 (24) corroborated the persistence of stable interactions between LA and the spike trimer (Movies S1,S2). The affinity of LA binding to the spike trimer will likely be higher than to the RBD alone, taking into account polar headgroup interactions with R408 and Q409 of the adjacent RBD (Fig. 1E). The resolution of the RBDs in our open S cryo-EM structure was insufficient to either assign, or rule out, a ligand-bound pocket (fig. S3). However, the slow off-rate observed with the RBD monomer (fig. S10) suggests that LA binding could be maintained when the S trimer transiently converts into the open conformation. This is supported by our observation that LA was retained during S purification in spite of S trimers adopting the open form ~30% of the time (fig. S2) and by our MD simulations with a modelled ligand-bound open spike trimer (Movie S3) in which all three LAs remained bound over 500 ns.

Next, we investigated the effect of LA in experiments using live SARS-CoV-2 virus to infect human epithelial cells. Remdesivir is an RNA-dependent RNA polymerase inhibitor and the first anti-viral drug showing benefit in the treatment of COVID-19 in clinical trials, albeit with considerable side effects at the doses required (25). LA supplementation at 50-100  $\mu$ M concentrations was previously shown to affect coronavirus entry and replication (10). We administered remdesivir at 20, 64 and 200 nM concentration, supplementing with 50  $\mu$ M LA (Fig. 2E). Our results revealed synergy, with the dose of remdesivir required to suppress SARS-CoV-2 replication markedly reduced by adding LA (Fig. 2E,F).



We superimposed our LA-bound structure on previous SARS-CoV-2 apo S structures in the closed conformation (7, 17) and identified a gating helix located directly at the entrance of the binding pocket (Fig. 3A-C). This gating helix, comprising Tyr365 and Tyr369, is displaced by about 6 Å when LA is bound, thus opening the pocket (Fig.3A,B). In the apo SARS-CoV-2 S trimer (7, 17), a gap between adjacent RBDs places the hydrophilic anchor residues ~10 Å away from the position of the LA headgroup (Fig. 3C). Upon LA binding, the adjacent RBD in the trimer moves towards its neighbor, and the anchor residues Arg408 and Gln409 lock down on the headgroup of LA (Fig. 3C,D). Overall, this results in a compaction of trimer architecture in the region formed by the three RBDs giving rise to a locked S structure (Fig. 3D, Movie S4).

We investigated whether the LA-binding pocket is conserved in the seven coronaviruses that infect humans (Fig. 4A, table S3). Sequence alignment shows that all residues lining the hydrophobic pocket and the anchor residues (Arg408/Gln409) in SARS-CoV-2 are fully conserved in SARS-CoV (Fig. 4A). Structural alignment of LA-bound RBDs within the trimer of SARS-CoV-2 and ‘apo’ SARS-CoV RBDs (19) reveals that the LA-binding pocket is present in SARS-CoV. The greasy tube is flanked by a gating helix as in SARS-CoV-2, with Arg395/Gln396 of SARS-CoV positioned 10Å and 11Å from the entrance, respectively, virtually identical to apo SARS-CoV-2 (Fig. 3C,4B). In MERS-CoV, the gating helix and hydrophobic residues lining the pocket are also present. Tyr365, Tyr369 and Phe374 are substituted by likewise hydrophobic leucines and a valine, respectively (Fig. 4A,C) (19). The Arg408/Gln409 pair is not conserved, however, we identify Asn501/Lys502 and Gln466 as potential anchor residues, located on a β-sheet and an α-helix within the adjacent RBD, up to 11Å away from the entrance (Fig. 4C). Thus, the greasy tube and hydrophilic anchor appear to be present in MERS-CoV, suggesting convergent evolution. In HCoV OC43, gating helix and hydrophobic residues lining the pocket are largely conserved, while

Tyr365, Tyr369 and Phe374 are replaced by methionines and alanine, respectively (Fig. 4A) (18). Arg413 is located on the same helix as Arg408/Gln409 in SARS-CoV-2 and could serve as a hydrophilic anchor (Fig. 4D). No gap exists in this presumed ‘apo’ form structure between the RBDs which appear already in the locked conformation (Fig. 4D, fig. S11 (18)). In HCoV HKU1, the hydrophobic residues are again largely conserved, but a charged residue (Glu375) is positioned directly in front of the entrance, obstructing access for a putative ligand (Fig. 4E) (26). The RBDs of HCoVs 229E and NL63 adopt a very different fold (fig. S13) (27, 28), and many of the LA-binding residues are not present (Fig. 4A), hampering predictions of a binding site for fatty acids. In summary, we find four molecular features mediating LA binding to SARS-CoV-2, and potentially also SARS-CoV and MERS-CoV S proteins: a conserved hydrophobic pocket, a gating helix, amino acid residues pre-positioned to interact with the LA carboxy headgroup, and loosely packed RBDs in the ‘apo’ form. In contrast, in each of the four common circulating HCoVs, it appears that one or more of these four architectural prerequisites are lacking in the S protein structures (Fig. 4, figs. S11,S12). LA binding to SARS-CoV-2 S triggers a locking down of the hydrophilic anchor and a compaction of the RBD trimer (Fig. 3C,D). In addition to stabilizing the closed conformation, this could also help stabilize the S1 region comprising the N-terminal domain and the RBD. The RBM, central to ACE2 binding, appears to be conformationally preorganized in our structure (Fig. 2C) indicating a generally more rigid RBD trimer when LA is bound. While direct crosstalk in between the LA-binding pocket and the RBM is not apparent from our structure (Fig. 2C), the conformational changes in the RBD trimer (Fig. 3) could impact ACE2 docking and infectivity as indicated by our SPR assays showing reduced levels of S binding in the presence of LA (Fig. 2D). The S protein's tight binding of LA originates from a well-defined size and shape complementarity afforded by the pocket (Fig. 1B,D). The LA-binding pocket thus presents a

promising target for future development of small molecule inhibitors that, for example, could irreversibly lock S in the closed conformation and interfere with receptor interactions. It is noteworthy in this context that a fatty acid binding pocket was exploited previously to develop potent small molecule anti-viral drugs against rhinovirus, locking viral surface proteins in a conformation incompatible with receptor binding (29, 30). These anti-virals were successful in human clinical trials (31, 32).

A recent proteomic and metabolomic study of COVID-19 patient sera showed continuous decrease of FFAs including LA (33). Lipid metabolome remodeling is a common element of viral infection (34, 35). For coronaviruses, the LA to arachidonic acid metabolic pathway was identified as central to lipid remodeling (10). We hypothesize that LA sequestration by SARS-CoV-2 could confer a tissue-independent mechanism by which pathogenic coronavirus infection may drive immune dysregulation and inflammation (35-37). Our findings provide a direct structural link between LA, COVID-19 pathology and the virus itself and suggest that both the LA-binding pocket within the S protein and the multi-nodal LA signaling axis, represent excellent therapeutic intervention points against SARS-CoV-2 infections.

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**Competing interests:** The authors declare competing interests. I.B and F.G. report shareholding in Imophoron Ltd. unrelated to this Correspondence. I.B. and D.F. report shareholding in Geneva Biotech Sàrl related to this Correspondence. Patent applications describing methods and material compositions based on the present observations have been filed.

**Data and materials availability:** Datasets generated during the current study have been deposited in the Electron Microscopy Data Bank (EMDB) under accession numbers EMD-11145 (C3 closed conformation), EMD-11144 (C1 closed conformation) and EMD-11146 (open conformation), and in the Protein Data Bank (PDB) under accession numbers: 6ZB5 (C3 closed conformation) and 6ZB4 (C1 closed conformation). Reagents are available from I.B. and C.S. under a material transfer agreement with the University of Bristol.

**Supplementary Materials:**

Materials and Methods

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References (41-63) are part of the Supplement and not cited in the Main Text.

## Figure Legends

**Figure 1. Cryo-EM structure of SARS-CoV-2 spike linoleic acid complex.** (A) Cryo-EM density of spike trimer (left). Monomers in cyan, green and pink, respectively. The structure in a cartoon representation in a front (middle) and top view (right). Bound LA illustrated as spheres colored in orange. One LA-binding pocket is boxed in red. (B) Composite LA-binding pocket formed by adjacent RBDs. Tube-shaped EM density is shown. (C) LC-MS of purified S. Chemical structure and molecular weight of LA (top), C4 column elution profile (middle) and ESI-TOF of wash solution (grey) and C4 peak elution fraction (black) with peak molecular weight indicated (bottom). (D) Hydrophobic LA-binding pocket in a surface representation illustrating excellent fit of bound LA (orange, sticks and balls representation). Blue and red indicate positive and negative surface charge, respectively. (E) LA interactions with amino acids in the binding pocket. The acidic LA headgroup is in the vicinity of an arginine (408) and a glutamine (409).

**Figure 2. Functional characterization of LA-bound SARS-CoV-2 spike.** (A) Insect cell (Hi5) expressed spike (dark blue bars), insect cell expressed RBD (light blue bars) and mammalian (HEK293) expressed spike (white bars) in competition ELISAs utilizing immobilized ACE2. Error bars: standard deviations, three replicates. (B) LA-bound SARS-CoV-2 spike protein interaction with ACE2 was analyzed by size exclusion chromatography evidencing complex formation. SEC profiles (left) for ACE2 (yellow, III), LA-bound spike (green, II) and a mixture of ACE2 and LA-bound spike (orange, I) are shown. Peak fractions (I.-III.) were analyzed by SDS-PAGE evidencing the expected proteins (right). (C) LA-bound S glycoprotein trimer top view with RBDs shown in cyan, green and pink respectively (left). In each RBD subunit the motif responsible for ACE2 binding (RBM) is in red, and LA is shown as spheres colored in orange. A close-up view

into the cyan RBD (right) shows that the RBM is fully ordered, and LA and RBM are not in direct contact. **(D)** SPR analysis of the binding of LA-bound spike trimer (orange curves) and apo spike trimer (green curves) to immobilized ACE2. Apo spike and LA-bound spike were diluted to concentrations of 40 nM and 160 nM, respectively. Black lines correspond to a global fit using a 1:1 binding model. **(E)** Synergistic effect of LA and remdesivir on SARS-CoV-2 viral replication. Effects of varying doses of remdesivir +/- 50  $\mu$ M LA on virus infection are shown. Human Caco-2 ACE2+ cells were infected with SARS-CoV-2 and then treated with varying doses of remdesivir +/- 50  $\mu$ M LA. At 96h post-infection, cells were fixed and infected cells detected by immunofluorescence assay using an anti-N antibody (green). Cell nuclei were stained by DAPI (blue). Representative images corresponding to the remdesivir dose range 20 – 200 nM are shown. **(F)** The amount of extracellular virus present in wells (n=3) at the dose combinations shown was determined by qRT-PCR.

**Figure 3. Comparison of LA-bound and apo S structures.** **(A)** Superimposition of LA-bound SARS-CoV-2 (cyan RBD) and the ligand-free ‘apo’ RBD (grey) (PDBID 6VXX, (7)). The gating helix at the entrance of the hydrophobic pocket moves by 6 Å in the presence of LA. Tyr365 and Tyr369 swing away avoiding clashes with LA (orange). Black arrows indicate the rearrangements. **(B)** The same structure as panel A rotated by 90° as indicated, showing the entrance of the hydrophobic pocket. **(C)** Formation of a composite LA-binding pocket by two adjacent RBDs in LA-bound S involves a ~5 Å movement of RBD2 (green) towards RBD1 (cyan) compared to apo S (grey). **(D)** Superimposition of the RBD trimer of apo S (grey) and LA-bound S (RBD1 cyan, RBD2 green, RBD3 pink, LA orange) is shown (left). The individual RBD trimers are depicted

for LA-bound S (right, top) and apo S (right, bottom) with RBDs boxed in black, highlighting the compaction of RBDs in the LA-bound S structure.

**Figure 4. Human coronavirus RBD architectures.** (A) Alignments of the seven CoV strains that can infect humans, highlighting conserved residues. Residues lining the hydrophobic pocket are underlaid (cyan). Gating helix residues are marked (purple). Residues positioned to interact with the LA polar headgroup are underlaid in green. Glu375 in HKU1 is underlaid in red (cf. panel E). (B) Superimposition of RBD1 of LA-bound SARS-CoV-2 (RBD2 in green) with RBD1 of ligand free ‘apo’ SARS-CoV (RBD1 and RBD2 magenta, PDBID 5X58 (19)) indicates a conservation of the composite binding pocket. (C) Superimposition of RBD1 of LA-bound SARS-CoV-2 (RBD2 is omitted for clarity) with RBD1 of MERS-CoV (RBD1 and RBD2 forest green, PDBID 5X5F (19)). (D) Superimposition of RBD1 of LA-bound SARS-CoV-2 (RBD2 in green) with RBD1 of OC43 (RBD1 and RBD2 purple, PDBID 6NZK, (18)). (E) Superimposition of LA-bound SARS-CoV-2 RBD with HKU1 RBD (brown, PDBID 5GNB (26)). LA is omitted in SARS-CoV-2 RBD for clarity.





## Supplementary Materials for

### Free fatty acid binding pocket in the locked structure of SARS-CoV-2 spike protein

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#### Other Supplementary Material for this manuscript includes the following:

Movies S1 to S4

MDAR Reproducibility Checklist (PDF)

## Materials and Methods

### Protein production.

*SARS-CoV-2 spike protein.* The pFastBacDual plasmid for SARS-CoV-2 S ectodomain for expression in insect cells (14) was kindly provided by Florian Krammer (Icahn School of Medicine, USA). In this construct, S comprises amino acids 1 to 1213 and is fused to a C-terminal thrombin cleavage site followed by a T4-foldon trimerization domain and a hexahistidine affinity purification tag. The polybasic cleavage site has been deleted (RRAR to A) in the construct (14). Protein was produced with the MultiBac baculovirus expression system (Geneva Biotech, Geneva, Switzerland) (41) in Hi5 cells using ESF921 media (Expression Systems Inc.). Supernatants from transfected cells were harvested 3 days post-transfection by centrifugation of the culture at 1,000g for 10 min followed by another centrifugation of supernatant at 5,000g for 30 min. The final supernatant was incubated with 7 ml HisPur Ni-NTA Superflow Agarose (Thermo Fisher Scientific) per 3 liters of culture for 1h at 4°C. Subsequently, a gravity flow column was used to collect the resin bound with SARS-CoV-2 spike protein, the resin was washed extensively with wash buffer (65 mM NaH<sub>2</sub>PO<sub>4</sub>, 300 mM NaCl, 20 mM imidazole, pH 7.5), and the protein was eluted using a step gradient of elution buffer (65 mM NaH<sub>2</sub>PO<sub>4</sub>, 300mM NaCl, 235mM imidazole, pH 7.5). Elution fractions were analyzed by reducing SDS-PAGE and fractions containing SARS-CoV-2 spike protein were pooled, concentrated using 50 kDa MWCO Amicon centrifugal filter units (EMD Millipore) and buffer-exchanged in phosphate-buffered saline (PBS) pH 7.5. Concentrated SARS-CoV-2 S was subjected to size exclusion chromatography (SEC) using a Superdex 200 increase 10/300 column (GE Healthcare) in PBS pH 7.5. Peak fractions from SEC were analyzed by reducing SDS-PAGE and negative stain electron microscopy (EM); fraction 7 was used for cryo-EM (fig.S1).

*Lipidex-treated SARS-CoV-2 spike protein.* Purified SARS-CoV-2 spike protein was treated with lipidex-1000 resin (Perkin Elmer; cat no. 6008301) according to published protocols (23, 42, 43). Briefly, S was incubated with lipidex-1000 resin pre-equilibrated in PBS pH 7.5 overnight at 4°C on a roller shaker. Subsequently, lipidex-treated S was separated from the resin using a gravity flow column. Integrity of the protein was confirmed by size exclusion chromatography (SEC) using a S200 10/300 increase column (GE Healthcare) and SDS-PAGE.

*ACE2 protein.* The gene encoding for the ACE2 ectodomain (amino acids 1 to 597) was codon optimized for insect cell expression, synthesized (Genscript Inc., New Jersey USA) and inserted into pACEBac1 plasmid (Geneva Biotech, Geneva, Switzerland). The resulting construct pACEBac1\_MelACE2his construct contains an N-terminal melittin signal sequence for secretion and a C-terminal octa-histidine affinity purification tag. ACE2 protein was produced and purified following the same protocol as for spike protein.

*Biotinylated ACE2 protein.* ACE2 was modified by inserting a synthetic DNA between the *StuI* and *HindIII* restriction sites in pACEBac1-MelACE2his giving rise to a modified C-terminus including a linker (amino acid sequence GGSGSG) followed by avi tag (amino acid sequence GLNDIFEAQKIEWHE), a second linker (amino acid sequence GGSGG) and an octa-histidine tag for purification. Avi-tagged ACE2 was produced using the same protocol as for ACE2 protein. Biotinylation was achieved by incubation with BirA in the presence of biotin according to established protocols (44). Remaining free biotin and BirA were removed by purifying biotinylated ACE2 using Ni-NTA Superflow Agarose followed by size exclusion chromatography (SEC) using a S200 10/300 increase column (GE Healthcare).

*Receptor Binding domain (RBD) and biotinylated RBD.* The gene encoding for the SARS-CoV-2 receptor binding domain (amino acids R319 to F541), fused at its N-terminus to the native spike signal sequence (amino acid sequence MFVFLVLLPLVSSQ), was codon optimized for insect cell expression, synthesized (Genscript Inc., New Jersey USA) and inserted into pACEBac1 plasmid (Geneva Biotech, Geneva, Switzerland). The resulting construct pACEBac1-RBDhis comprises a C-terminal octa-histidine affinity purification tag. Protein was produced and purified as described for spike trimer. Biotinylated RBD was generated by adding an avi tag for BirA mediated biotinylation as described above for biotinylated ACE2. Lipidex-treated biotinylated RBD was then prepared as described above for lipidex-treated S.

#### Negative stain sample preparation and microscopy

4  $\mu$ L of 0.05 mg/mL SARS-CoV-2 spike protein was applied onto a freshly glow discharged (1 min at 10 mA) CF300-Cu-50 grid (Electron Microscopy Sciences), incubated for 1 min, and manually blotted. 4  $\mu$ L of 3% Uranyl Acetate was applied onto the same grid and incubated for 1 min before the solution was blotted off. The grid was loaded onto a FEI Tecnai 12 120 kV BioTwin Spirit TEM. Images were acquired at a nominal magnification of 49,000x.

#### Cryo-EM sample preparation and data collection

4  $\mu$ L of 1.25 mg/mL SARS-CoV-2 spike protein was loaded onto a freshly glow discharged (2 min at 4 mA) Quantifoil R1.2/1.3 carbon grid (Agar Scientific), blotted using a Vitrobot MarkIV (Thermo Fisher Scientific) at 100% humidity and 4°C for 2 s, and plunge frozen. Data were acquired on a FEI Talos Arctica transmission electron microscope operated at 200 kV and equipped with a Gatan K2 Summit direct detector and Gatan Quantum GIF energy filter, operated in zero-loss mode with a slit width of 20 eV using the EPU software.

Data were collected in super-resolution at a nominal magnification of 130,000x with a virtual pixel size of 0.525 Å. The dose rate was adjusted to 6.1 counts/physical pixel/s. Each movie was fractionated in 55 frames of 200 ms. 3289 micrographs were collected in a single session with a defocus range comprised between -0.8 and -2  $\mu$ m.

#### Cryo-EM data processing

The dose-fractionated movies were gain-normalized, aligned, and dose-weighted using MotionCor2 (45). Defocus values were estimated and corrected using CTFFIND4 (46). 611,879 particles were automatically picked using Relion 3.0 software (47). Reference-free 2D classification was performed to select well-defined particles, after four rounds of 2D classification a total of 386,510 good particles were selected for further 3D classification. An initial model was generated using 50,000 particle images in Relion 3.0, and the selected particles from 2D classification were subjected to 3D classification using 8 classes. Classes 4 and 6 (fig. S2), showing prominent features representing a total of 202,082 particles were combined and used for 3D refinement. The 3D refined particles were then subjected to a second round of 3D classification using 5 classes. Class 4 and 5 were combined for the closed conformation map, class 3 represented the open conformation, comprising 136,405 and 57,990 particles respectively. The selected maps were subjected to 3D refinement without applying any symmetry with respective 3D models. The

maps were subsequently subjected to local defocus correction and Bayesian particle polishing in Relion 3.0. Global resolution and B factor ( $-89 \text{ \AA}^2$  and  $-116 \text{ \AA}^2$  for closed and open maps respectively) of the map were estimated by applying a soft mask around the protein density, using the gold standard Fourier shell correlation (FSC) = 0.143 criterion, resulting in an overall resolution of  $3.03 \text{ \AA}$  and  $3.7 \text{ \AA}$  respectively. The open map was imported into Relion 3.1 software, where it was further corrected for higher-order aberrations and magnification anisotropy. This yielded a final resolution of  $3.5 \text{ \AA}$  (B factor of  $-87 \text{ \AA}^2$ ). C3 symmetry was applied to the closed conformation map using Relion 3.0, followed by 3D classification using 3 classes. Class 3 with 217,815 particles was selected for CTF refinement and Bayesian polishing, yielding a final resolution of  $2.85 \text{ \AA}$  (B factor of  $-86.8 \text{ \AA}^2$ ). Local resolution maps were generated using Relion 3.0 (fig. S3).

### Cryo-EM model building and analysis

UCSF Chimera (48) and Coot (49) were used to fit atomic models (PDBID 6VXX, (7)) into the cryo-EM map. The model was subsequently manually rebuilt using Coot and the closed conformation map. This closed conformation model was used to build features specific of the open conformation map and to further improve the model by using the C3-symmetrized map. To guide the model building, sharpened (50) and unsharpened maps were used in different steps of the process. N-linked glycans were hand-built into the density where visible, and restraints for non-standard ligands were generated with eLBOW (51). The model for the closed conformation was real space refined with Phenix (52) and the quality was additionally analyzed using MolProbity (53) and EMRinger (54), to validate the stereochemistry of the components. The quasi-atomic model of the open conformation was generated by first fitting the atomic model of the closed conformation into the open cryo-EM map using UCSF Chimera. We then used COOT and UCSF Chimera to move one RBD into the open conformation, by aligning this RBD to the atomic model of a published open form of SARS-CoV-2 S (PDBID 6VSB, (17)). Finally, this open model was fitted into the cryo-EM open map with COOT and UCSF Chimera. Figures were prepared using UCSF Chimera and PyMOL (Schrödinger, Inc.).

### Masked 3D classification in Relion

The refined C3 particles stack was expanded 3-fold according to C3 symmetry in Relion. The symmetry expanded particle stack was then used as input for the masked 3D classification with the focus mask corresponding to NTD-RBD region created by one NTD and one RBD from neighbouring subunits. The same procedure was performed with refined C1 particles without particle expansion, applying 3 masks, one for each NTD-RBD pair. Masked 3D classification was performed without alignment using 5 classes for C3 particle and 3 classes for C1 particle data sets. Visual inspection of the 3D classes showed ~80% of the RBD's clustered in class 3 in C3 and in class 1 in C1 with LA bound in the hydrophobic pocket.

### Mass spectrometry analysis

For mass spectrometry analysis, a Bruker maXis II ETD quadrupole-time-of-flight instrument with electrospray ionization (ESI) coupled to a Shimadzu Nexera HPCL was used. In order to extract the fatty acids from the protein sample, a chloroform extraction protocol was performed. For this,

100 µl of the protein sample was mixed with 400 µl chloroform for 2 hours on a horizontal shaker in a teflon-sealed glass vial at 25°C. The organic phase was then transferred to a new glass vial and the chloroform was evaporated for 30 min in a desiccator. Subsequently, 50 µl of a 20% (v/v) acetonitrile solution was added to dissolve the fatty acids. From this solution, a 1:100 dilution in 20% (v/v) acetonitrile was prepared and 20 µl were injected for LC-MS analysis. The samples were passed over a Phenomenex C4 Aeris column (100 × 2.1 mm, 3.6 µm, 200 Å) heated to 50°C using a gradient of 20% A to 98% B in 5 min (solvent A: H<sub>2</sub>O + 0.1% formic acid; solvent B: ACN + 0.1% formic acid). The system was operated with Bruker's O-TOF Control (V4.1) and Hystar (V4.1) software and data analysis as well as data post-processing was performed with Bruker's DataAnalysis software (V4.4, SR1).

### ELISA activity assay

The SARS-CoV-2 sVNT kit was obtained from GenScript Inc. (New Jersey, USA) for ELISA activity assays. Serial dilution series were prepared (from 0-4096 nM) of purified SARS-CoV-2 spike proteins and RBD in PBS pH 7.5. This dilutions series was mixed with the same amount of HRP-RBD and incubated at 37°C for 30 min. The mixtures were then added to ELISA plate wells, coated with ACE2 according to the manufacturer's protocol. Triplicates of each sample were made. The ELISA plate was then incubated at 37°C for 15 min and subsequently washed 4 times with wash buffer. The signal was then developed by adding TMB solution to each well, incubating 15 minutes in the dark, followed by adding stop solution. The absorbance at 450 nm was immediately recorded. The data was plotted using Microsoft excel. The standard deviation of triplicates was added as error bars.

### SARS-CoV-2 spike / ACE2 interaction analysis, size exclusion chromatography (SEC)

Purified SARS-CoV-2 spike and ACE2 proteins were combined in PBS pH 7.5 at a molar ratio of 1:1.5 spike trimer to ACE2 monomer. The mixture was incubated on ice for 2 hours and subjected to SEC using a Superdex 200 increase 10/300 column (GE Healthcare) equilibrated in PBS pH 7.5. Purified SARS-CoV-2 spike protein and ACE2 proteins were individually run on the same column in the same buffer as controls. The contents of peak fractions were analyzed by reducing SDS-PAGE.

### Surface plasmon resonance (SPR) experiments

Interaction experiments using surface plasmon resonance (SPR) were carried out with a Biacore T200 system (GE Healthcare) according to the manufacturer's protocols and recommendations. For RBD / ACE2 interaction measurements, purified biotinylated ACE2 was immobilized on a streptavidin coated (SA) chip (GE Healthcare) at ~300 response units (RUs). Purified RBD was serially diluted and injected at concentrations 80 nM, 120 nM, 140 nM and 160 nM. Measurements were carried out in triplicates. For measuring ACE2 interactions with S and lipidex-treated S, respectively, purified biotinylated ACE2 was immobilized at ~50 RUs and purified proteins serially diluted and injected at concentrations of 40 nM, 60 nM, 80 nM, 120 nM and 160 nM. For LA / RBD measurements, biotinylated RBD was immobilized at ~3800 RUs as required, according to our calculations, for a sufficiently prominent signal upon binding of the small molecule LA (MW 280 Da). LA was purchased as a sodium salt (Sigma Aldrich, cat no. L8134) and dissolved



in PBS pH 7.5 at a concentration of 10  $\mu$ M, serially diluted and injected at concentrations 4  $\mu$ M, 6  $\mu$ M, 8  $\mu$ M and 10  $\mu$ M. Running buffer for all measurements was PBS buffer pH 7.5. Sensorgams were analyzed and  $K_D$ ,  $k_{on}$  and  $k_{off}$  values in all SPR experiments determined with the Biacore Evaluation Software (GE Healthcare), fitting the raw data using a 1:1 binding model.

### Live SARS-CoV-2 experiments

*Cell culture.* A Vero E6 cell line modified to constitutively express the serine protease TMPRSS2 (Vero E6/TMPRSS2; (9) (obtained from NIBSC, UK) and the human gut epithelial cell line Caco-2 expressing ACE2 (Caco-2-ACE2) (a kind gift of Dr Yohei Yamauchi, University of Bristol) were cultured at 37°C in 5% CO<sub>2</sub> in Dulbecco's modified Eagle's medium plus GlutaMAX (DMEM, Gibco, ThermoFisher) supplemented with 10% fetal bovine serum (FBS, Gibco, ThermoFisher) and 0.1 mM non-essential amino acids (NEAA, Sigma Aldrich).

*SARS-CoV-2 viral propagation.* A stock of infectious virus was produced by inoculation of Vero E6/TMPRSS cells with the SARS-CoV-2 isolate SARS-CoV-2/human/Liverpool/REMQRQ0001/2020 (55) in infection medium (Eagle's minimum essential medium plus GlutaMAX (MEM, Gibco, ThermoFisher) supplemented with 2% FBS and NEAA). Cells were incubated at 37°C in 5% CO<sub>2</sub> for 72 hours before being harvested and filtered through a 0.2  $\mu$ m filter. The viral titer was determined by TCID<sub>50</sub> on Vero E6 cells as previously described (56).

*SARS-CoV-2 infection assay.* Caco-2-ACE2 cells were seeded for 18 hours in DMEM in  $\mu$ Clear 96-well Microplates (Greiner Bio-one). The culture supernatant was removed and cells were infected with SARS-CoV-2 diluted in infection medium to a MOI of 0.1 for 1 hour. The virus was removed and replaced with infection medium containing eight-fold serial dilutions of LA, remdesivir (RMD; Cambridge Bioscience, UK) or LA+RMD. After 96 hours incubation at 37°C in 5% CO<sub>2</sub>, supernatants were collected for qRT-PCR and cells fixed in 4% PFA for 60 minutes for image analysis. All work with infectious SARS-CoV-2 virus was conducted in a Class III microbiological safety cabinet in a containment level 3 facility at the University of Bristol.

*Cell viability assay.* Cell viability and compound toxicity were determined by MTT assay. Samples were treated identically to viral infection assays, with the exclusion of the viral inoculation step. After 96 hours incubation at 37°C, media was removed and replaced by Thiazolyl Blue Tetrazolium Bromide (MTT; Sigma Aldrich) solution (1 mg/ml) and incubated for 3 hours at 37°C. The MTT reagent was then removed and cells lysed by addition of 100% ethanol. Samples were analyzed by reading the absorbance at 600 nm.

*qRT-PCR.* Culture supernatants were collected and RNA extracted using the QIAamp Viral RNA Isolation kit (Qiagen) according to the manufacturer's instructions with elution of RNA in 60  $\mu$ l of AVE solution. 5  $\mu$ l of each sample was used for qRT-PCR analysis using a TaqPath™ 1-Step RT-qPCR Master Mix, CG (Applied Biosystems, ThermoFisher) following the manufacturer's instructions and the previously described SARS-CoV-2 E gene primer set (57) using a Mx3005P Real-Time PCR System (Agilent). SARS-CoV-2 RNA genome equivalence was determined using the MxPro qPCR Software (Agilent) and RNA extracted from titered virus and a AccuPlex™ SARS-CoV-2 Reference Material Kit (SeraCare, Milford, US) as standards.

*Immunofluorescence analysis.* Fixed cells were stained for DAPI (Sigma Aldridge) and SARS-CoV-2 nucleocapsid (N) protein (200-401-A50, Rockland) following permeabilization with

Triton-X100 and blocking with BSA. Images were acquired on the ImageXpress Pico Automated Cell Imaging System (Molecular Devices) using the 10X objective. Stitched images of 9 fields covering the central 36% of the well were analyzed for infected cells using Cell Reporter Xpress software (Molecular Devices). Briefly, cell number was determined by automated counting of DAPI stained nuclei, infected cells are determined as those cells in which positive N staining was detected associated with a nuclei. The percentage of infected cells relative to control wells in which no drug was added (virus only) were calculated and variable slope non-linear fit curves were assigned using GraphPad Prism v8.4.3.

## Computational Studies

### Modelling

Loops for the unstructured regions of the locked (linoleic acid bound) and open (apo) cryo-EM structures were built using UCSF Chimera (48). Disulphide bonds within reasonable reach were reconstructed (42 for the closed structure and 43 for the open) and each chain sequence was used in an EBI-blast check to verify wild type spike sequence post build. Procheck (58) was then used to check the quality of the resulting structure prior to simulation. Acptype (59) was used to prepare the topologies for the linoleic acid.

### Molecular Dynamics Simulations

*Simulation details:* All simulations were performed under the AMBER99SB-ILDN (60-62) forcefield as NPT ensembles at 310 K using periodic boundary conditions. Hydrogen atoms, consistent to pH 7, were added to the complex. Short range electrostatic and van der Waals interactions were truncated at 1.4 nm while long range electrostatics were treated with the particle-mesh Ewald method and a long-range dispersion correction applied. A simulation box extending 2 nm from the protein was filled with TIP3P waters and 150 mM Na and Cl ions added to attain a neutral charge overall. Pressure was controlled by the Berendsen barostat and temperature by the V-rescale thermostat. The simulations were integrated with a leap-frog algorithm over a 2 fs time step, constraining bond vibrations with the P-LINCS method. Structures were saved every 0.1 ns for analysis in each of the simulations over 100 ns. Simulation data were accumulated on the Bristol supercomputer BlueCrystal Phase 4, the BrisSynBio BlueGEM, and the UK supercomputer, ARCHER.

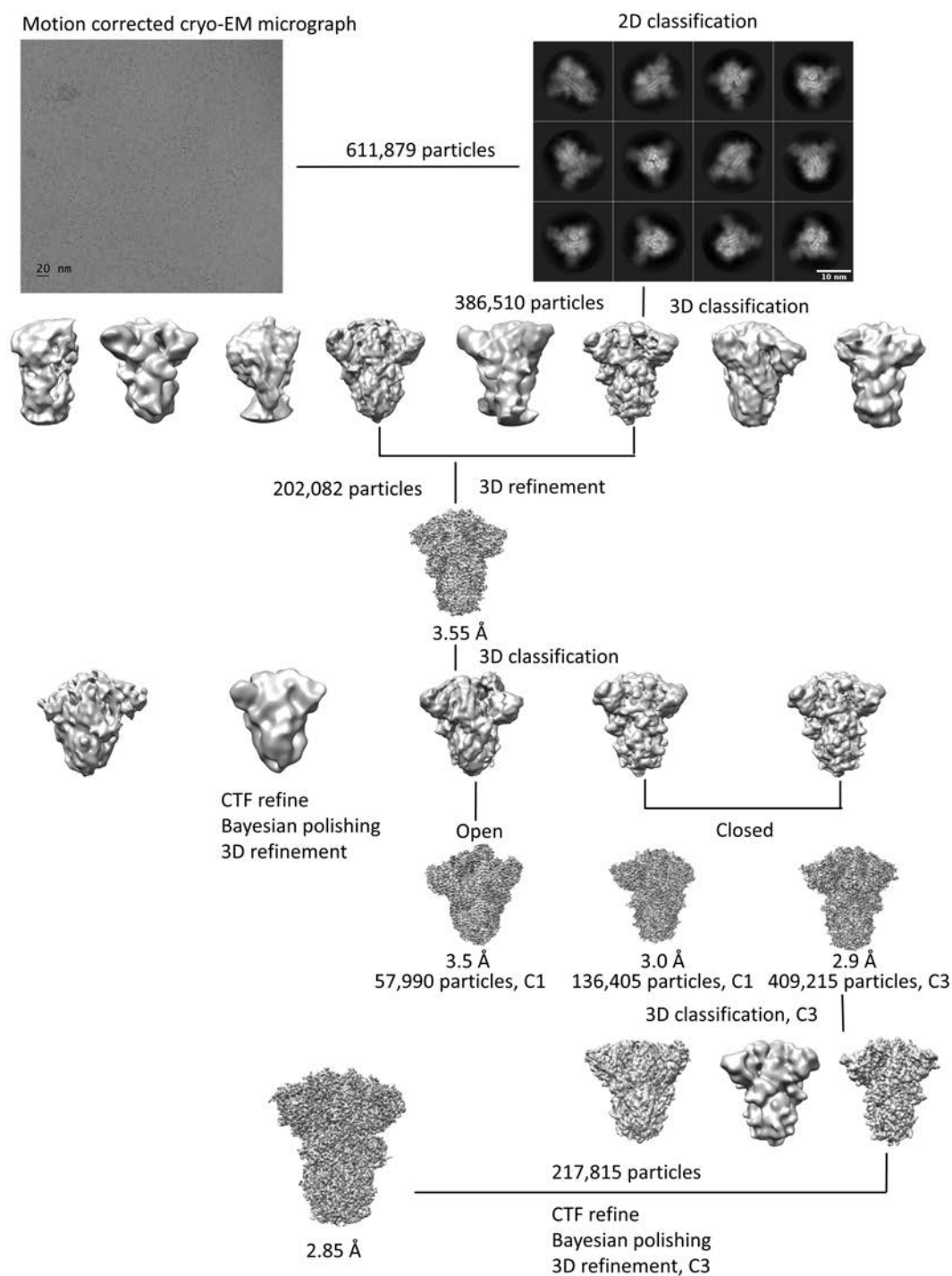
*Software.* The GROMACS-2019.2 (24) suite of software was used to set up and perform the molecular dynamics simulations and analyses for BlueGEM and BlueCrystal Phase 4 runs and GROMACS-2019.1 (24) for the ARCHER runs. Molecular graphics manipulations and visualisations were performed using VMD-1.9.1 (63) and Chimera-1.10.2 (48) and movies made using VMD (63).

**Fig. S1.**

**Purification and quality control of SARS-CoV-2 spike protein.** (A) Size-exclusion chromatogram of affinity-purified SARS-CoV-2 spike protein using a Superdex 200 column. Absorption was detected at 280 nm (blue line) and 260 nm (red line). Peak fractions are indicated. The first peak at 8.6 mL elution volume corresponds to the void volume of the column comprising negligible amounts of spike protein as confirmed by the SDS-PAGE analysis in panel B (fractions 1 and 2). The spike trimer elutes at 10.8 mL. (B) SDS PAGE analysis of the SEC fractions from panel A. Lane 1: input fraction, lane 2: molecular weight marker, lane 3-15: fractions 1 to 13 from SEC. (C) Negative stain EM of SEC peak fraction 7 (scale bar: 100 nm). In panels A and B peak fraction 7 is highlighted with a red box; this fraction was used for negative stain EM and cryo-EM.

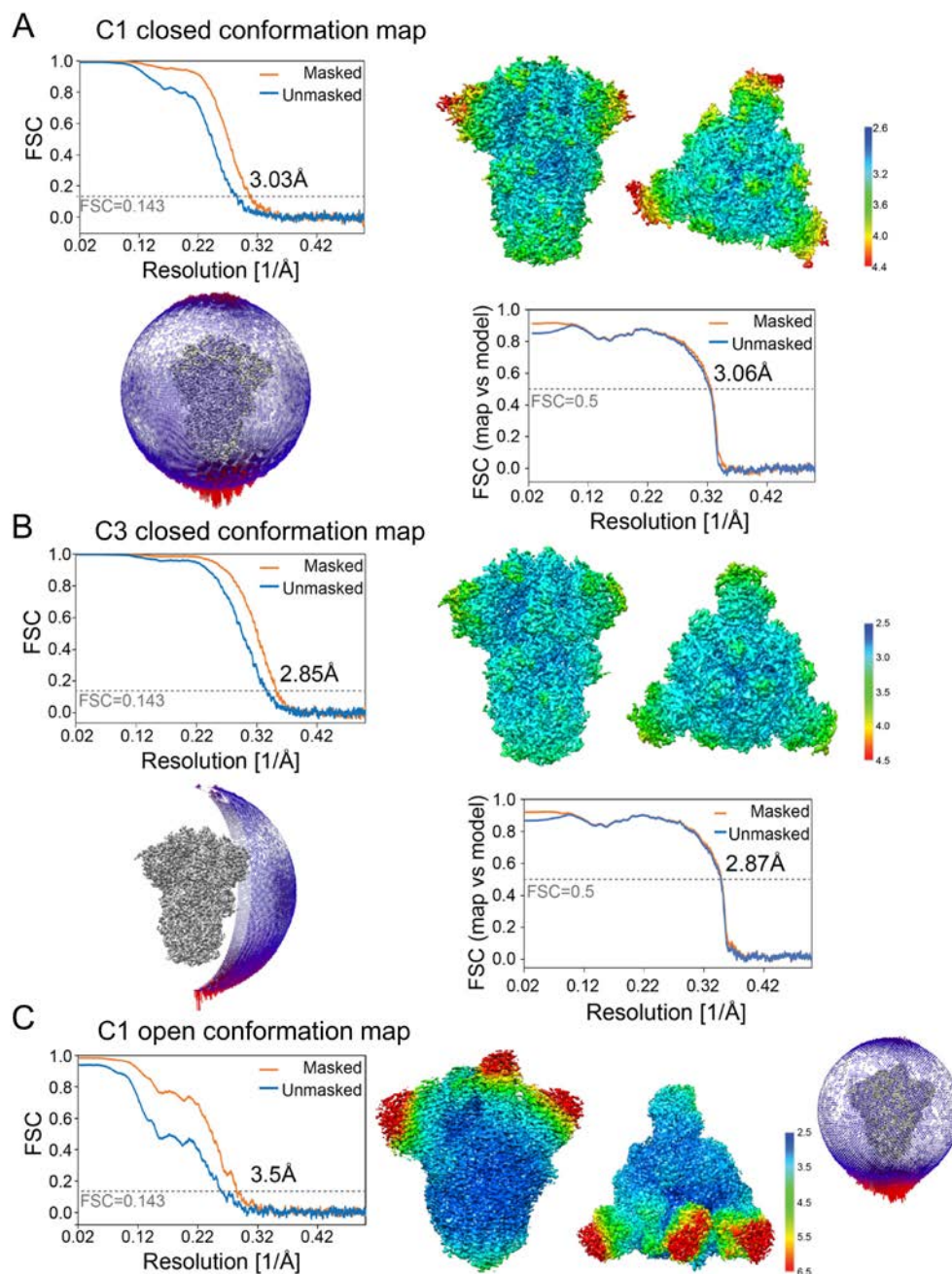


**Fig. S2.**



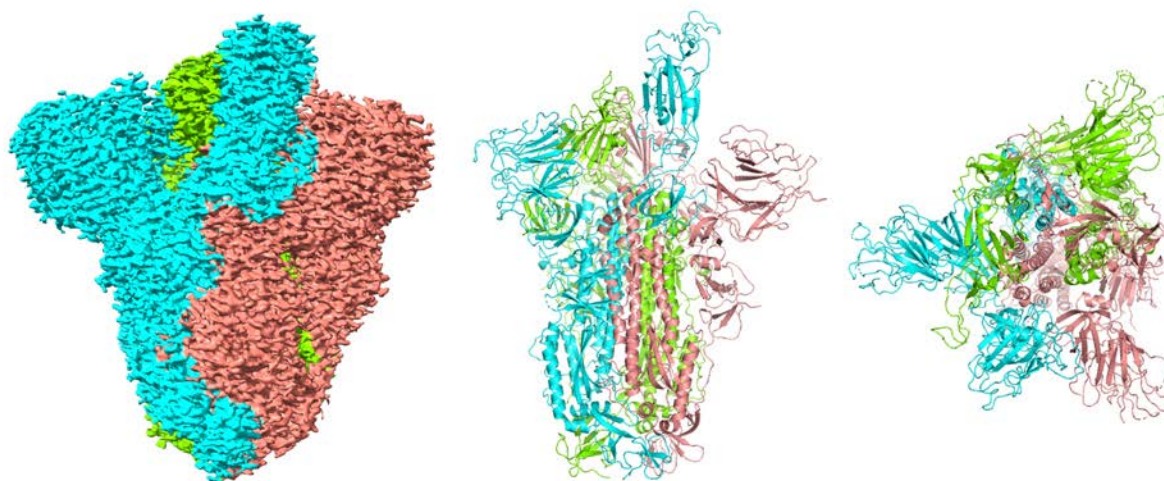
**Cryo-EM image processing workflow.** A motion-corrected cryo-EM micrograph is shown (scale bar 20 nm), reference-free 2D class averages (scale bar 10 nm), 3D classification and refinement resulting in cryo-EM maps corresponding to the open conformation and the closed conformation (not symmetrized and C3 symmetrized).

**Fig. S3.**



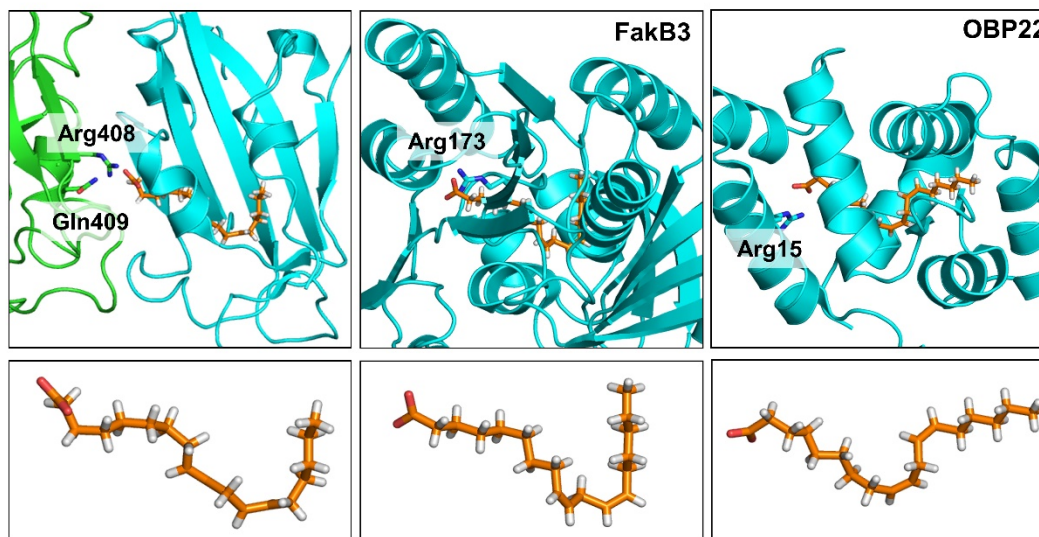
**Cryo-EM structure validation.** Top left: Fourier Shell Correlation (FSC) curve after gold standard refinement. Top right: Cryo-EM reconstruction colored according to the local resolution from a side and top view. Below left: Orientation distribution of views that contributed to this map. Longer red rods represent orientations that comprise more particles. Below right: Cross-validation FSC curves for the refined model versus the final masked and unmasked maps, shown for (A) the closed unsymmetrized C1 map (B) the closed C3-symmetrized map and (C) the open conformation map. For the open conformation, the views distribution is shown on the right, next to the local resolution map.

**Fig. S4.**



**Cryo-EM structure of SARS-CoV-2 S in the open conformation.** The 3.5 Å cryo-EM density of the SARS-CoV-2 spike trimer is shown (left). Monomers are colored in cyan, green and pink, respectively. A quasi-atomic model is depicted in a cartoon representation in a front (middle) and top view (right) using the same colors (c.f. Fig.1). RBDs were placed as rigid bodies, and LA was not included in the model.

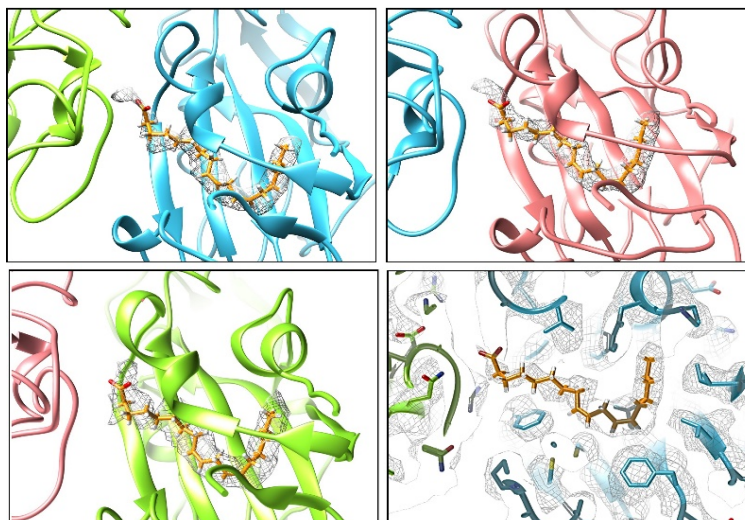
Fig. S5.



**LA binding protein complexes.** The structures of LA bound to SARS-CoV-2 S protein (this study, left), *Streptococcus pneumoniae* Fatty Acid Kinase (Fak) B3 (PDBID 6CNG (20), middle) and *Aedes aegypti* Odorant Binding Protein 22 (OBP22) (PDBID 6OGH, (21), right) are shown for comparison (top panel). Amino acids interacting with the polar headgroup of LA are labelled. Despite markedly different protein architectures, the conformation adopted by the LA in each complex is similar, featuring a pronounced kink in the structures (close-up views below).

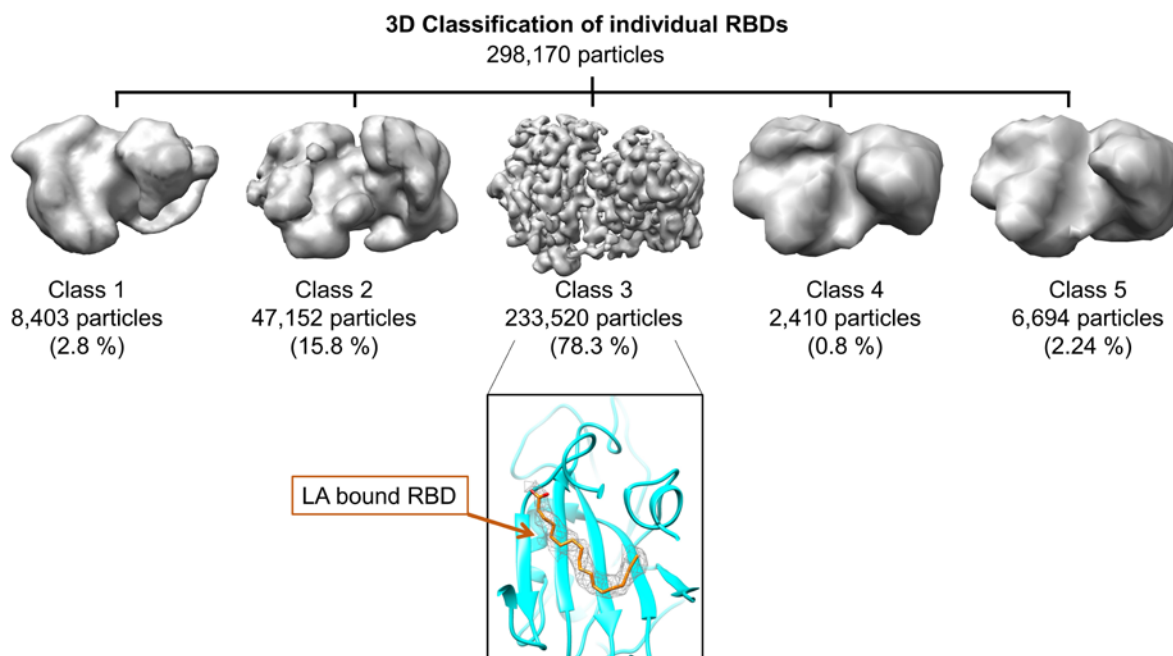


**Fig. S6.**



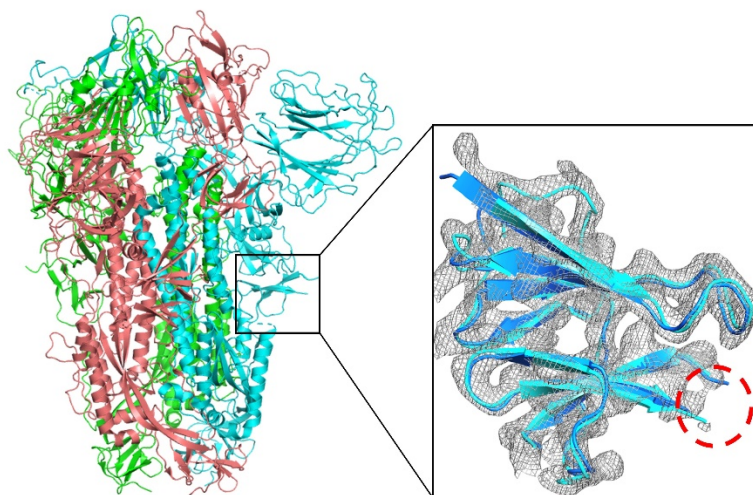
**LA ligands bound to the SARS-CoV-2 spike RBDs.** The three independent RBDs present in SARS-CoV-2 spike trimer are shown. Processing and refinement in C1 (no symmetry applied) results in tube-shaped density within all three RBDs, indicating that a LA ligand is present in each fatty acid-binding pocket. EM density is depicted as a mesh colored in grey. RBDs are colored cyan, green and pink (c.f. Figure 1). LA ligand is shown as sticks colored in orange. The density of amino acid residues in the binding pocket surrounding LA in the C3 structure is shown for comparison in a clipped view (bottom right).

**Fig. S7.**



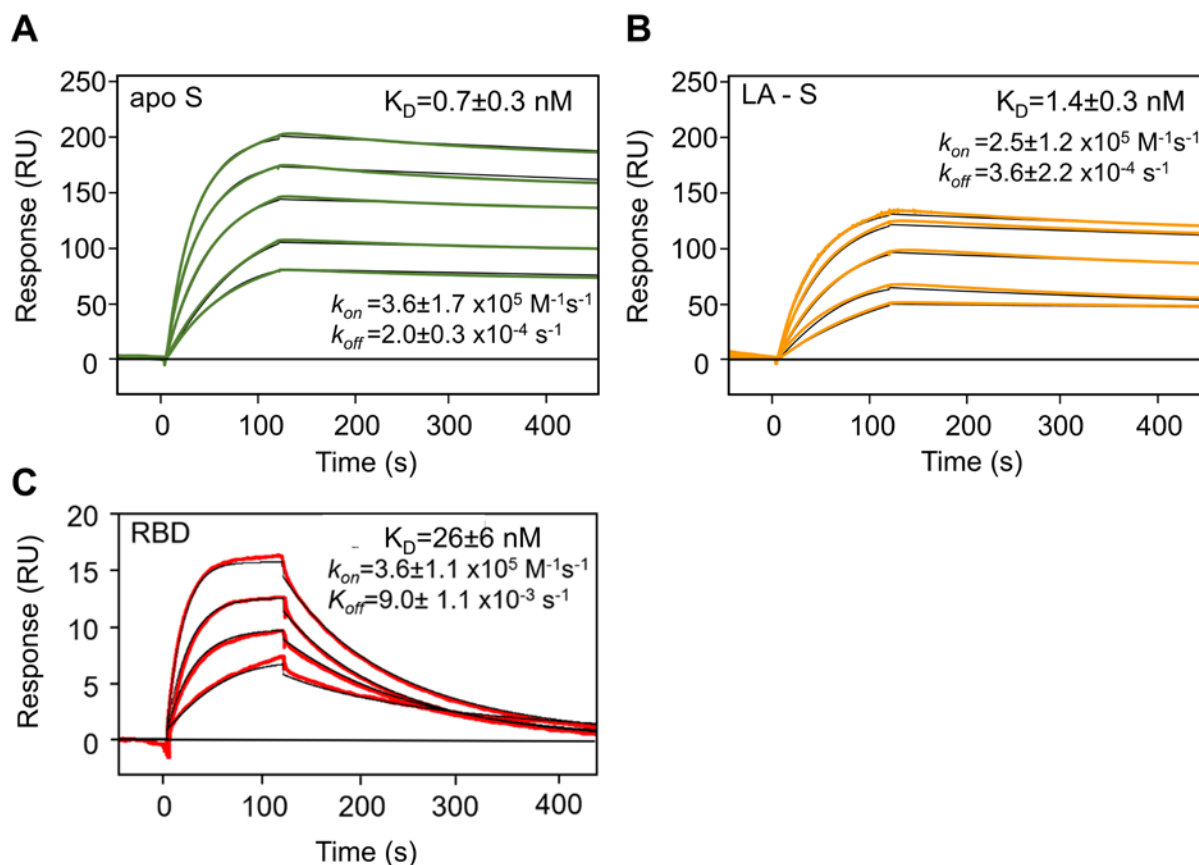
**Masked 3D classification focusing on the Receptor Binding Domain of the S glycoprotein into 5 classes.** Class 3 comprised 78.3% of all RBDs. This class presents LA bound RBD. The other 3D classes did not reach sufficient resolution to determine the presence or absence of LA in the RBD reconstructions.

**Fig. S8.**



**Polybasic cleavage site deletion in SARS-CoV-2 spike.** The construct used in this study has a RRAR to A deletion in the polybasic cleavage site (boxed in black). This site is part of a flexible loop in the S protein which is not observed by cryo-EM (circled in red in close-up view). Comparison of the LA-bound SARS-CoV-2 spike protein (cyan) and the ‘apo’ form (dark blue, PDBID 6VXX, RRAR->SGAG (7)) shown in a close up view superimposed on cryo-EM density (grey mesh) evidences that the structures are virtually identical in this region.

Fig. S9.



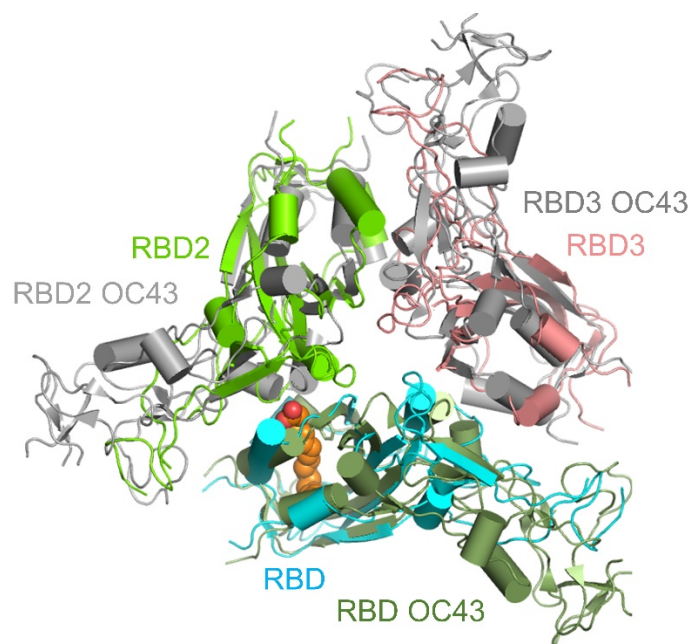
**Binding of spike glycoprotein and RBD to immobilized ACE2 ectodomain by surface plasmon resonance (SPR).** Apo spike glycoprotein (A) and LA-bound spike (B) were diluted to concentrations between 40 nM and 160 nM and flowed over 50 RU of biotinylated ACE2 immobilized on a streptavidin-coated sensor chip. Black lines correspond to a global fit of the data using a 1:1 binding model. Each experiment was repeated independently three times. All protein concentrations were used to calculate the  $K_D$ ,  $k_{on}$  and  $k_{off}$  values. For the RBD (C), 300 RU ACE2 were immobilized, and RBD concentrations from 80 nM to 160 nM were flowed over the ACE2 surface.



**Fig. S10.**

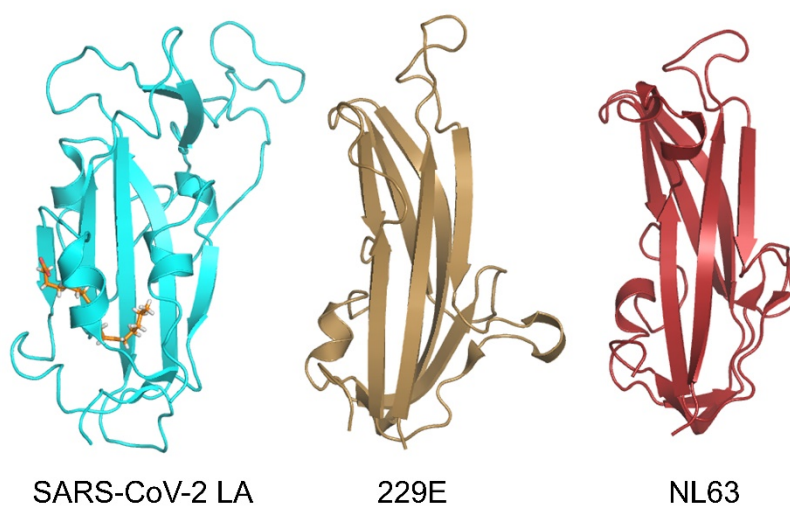
**Binding of LA to immobilized RBD by surface plasmon resonance (SPR).** LA was diluted to concentrations between 4  $\mu\text{M}$  and 10  $\mu\text{M}$  and flowed over 3,800 RU of biotinylated and lipidex-treated RBD immobilized on a streptavidin-coated sensor chip. Black lines correspond to a global fit of the data using a 1:1 binding model. Each experiment was repeated independently three times. All LA concentrations were used to calculate the  $K_D$ ,  $k_{\text{on}}$  and  $k_{\text{off}}$  values.

**Fig. S11.**



**Superimposition of RBDs in OC43 S protein trimer and LA-bound SARS-CoV-2 S.** The OC43 RBD colored in dark green and the LA-bound SARS-CoV-2 RBD colored in cyan were used for structure alignment. Two further RBDs in the trimer in OC43 S are colored in grey. Corresponding RBDs in the LA-bound SARS-CoV-2 S are colored in green and pink (c.f. Fig. 1). The three RBDs of OC43 are locked in a tightly packed conformation with close contacts at the RBD-RBD interfaces (PDBID 6NZK (18)).

Fig. S12.



**Spike protein RBD structures.** LA-bound SARS-CoV-2 S RBD (cyan, this study, left) and RBDs of commonly circulating human coronaviruses 229E (PDBID 6U7H (27), middle) and NL63 (PDBID 5SZS (28), right) are shown. The RBD architectures of 229E and BL63 are substantially different.

**Table S1.**  
**Cryo-EM data collection and refinement statistics.**

	<b>Closed conformation, C3 symmetrized</b>	<b>Closed conformation, C1</b>	<b>Open conformation, C1</b>
Voltage (kV)	200	200	200
Magnification (nominal)	130,000	130,000	130,000
Pixel size (Å/pix)	1.05 (0.525)	1.05 (0.525)	1.05 (0.525)
Flux (e <sup>-</sup> /pix/sec)	6.1	6.1	6.1
Frames per exposure	55	55	55
Exposure (e <sup>-</sup> /Å <sup>2</sup> )	60.5	60.5	60.5
Defocus range (μm)	-0.8 to -2	-0.8 to -2	-0.8 to -2
Micrographs collected	3289	3289	3289
Particles final	217,815	136,405	57,990
Map sharpening B-factor (Å <sup>2</sup> )	-86.8	-89	-87
Masked resolution at 0.143 FSC (Å)	2.85	3.03	3.5

**Refinement**

	<b>Closed conformation, C3 symmetrized</b>	<b>Closed conformation, C1</b>
<b>Composition</b>		
Amino acids	3096	3133
Glycans	26	27
Ligands	3	3
RMSD bonds (Å)	0.013	0.008
RMSD angles (°)	0.843	0.807
<b>Mean B-factors (Å<sup>2</sup>)</b>		
Amino acids	25.25	32.78
Ligands	36.91	38.86
<b>Ramachandran</b>		
Favoured (%)	92.20	90.17
Allowed (%)	7.80	9.66
Outliers (%)	0.00	0.16
Rotamer outliers (%)	3.27	5.84
Clash score	4.16	4.26
C-beta outliers (%)	0.00	0.00
CaBLAM outliers (%)	3.46	4.31
CC (mask)	0.84	0.84
MolProbity score	2.07	2.33
EMRinger score	3.59	3.79
Model resolution (Å) 0.5 FSC threshold	2.9	3.1

**Table S2.**  
**N-linked glycosylation sites in the SARS-CoV-2 spike protein**

<b>WT SARS-CoV-2 spike *</b>	<b>Recombinant SARS-CoV-2 spike expressed in</b>	
<b>Predicted (UNIPROT)</b>	<b>Freestyle 293F (7) **</b>	<b>Hi5 (this study) **</b>
N <sub>17</sub> LT		N <sub>17</sub> LT
N <sub>61</sub> VT	N <sub>61</sub> VT	N <sub>61</sub> VT
N <sub>74</sub> GT		
N <sub>121</sub> NA #		
N <sub>122</sub> AT	N <sub>122</sub> AT	N <sub>122</sub> AT
N <sub>149</sub> KS		
N <sub>165</sub> CT	N <sub>165</sub> CT	N <sub>165</sub> CT
N <sub>234</sub> IT	N <sub>234</sub> IT	N <sub>234</sub> IT
N <sub>282</sub> GT	N <sub>282</sub> GT	N <sub>282</sub> GT
N <sub>331</sub> IT	N <sub>331</sub> IT	N <sub>331</sub> IT
N <sub>343</sub> AT	N <sub>343</sub> AT	N <sub>343</sub> AT
N <sub>370</sub> SA #		
N <sub>603</sub> TS	N <sub>603</sub> TS	
N <sub>616</sub> CT	N <sub>616</sub> CT	N <sub>616</sub> CT
N <sub>657</sub> NS	N <sub>657</sub> NS	
N <sub>709</sub> NS	N <sub>709</sub> NS	N <sub>706</sub> NS
N <sub>717</sub> FT	N <sub>717</sub> FT	N <sub>714</sub> FT
N <sub>801</sub> FS	N <sub>801</sub> FS	N <sub>798</sub> FS
N <sub>1074</sub> FT	N <sub>1074</sub> FT	N <sub>1071</sub> FT
N <sub>1098</sub> GT	N <sub>1098</sub> GT	N <sub>1095</sub> GT
N <sub>1134</sub> NT	N <sub>1134</sub> NT	N <sub>1131</sub> NT
N <sub>1158</sub> HT		
N <sub>1173</sub> AS		
N <sub>1194</sub> ES		
<p>* YP_009724390.1</p> <p>**Sites lacking glycosylation in cryo-EM maps are omitted (boxes colored in grey).</p> <p># Predicted based on SARS-CoV spike protein (7)</p>		

Table S3.

Alignment of coronavirus S protein sequences (S-CryoEM denotes construct in this study)

	1	10	20	30
S-CryoEM	....MFVF	LVLLPL.V.....	SSQCVNL..TT..R....	TQLP...PAY..TN
SARS-CoV-2	....MFVF	LVLLPL.V.....	SSQCVNL..TT..R....	TQLP...PAY..TN
SARS-CoV	....MFIF	LVLLPL.T.....	SGSDDLDR...CTTFD...	DVQA...PNYTQHT
MERS-CoV	MIHS	VFLLMFLL	TPTESYVDVGPDS.VKSACIEV.DIQQTFF.....	DKTW...PRP.IDV
HCoV-229E	....			
HCoV-OC43	....MFLI	LLISLPTA.FAVIGDL....	KCPLDTSYKGTEN..NKDTGPPFISTDTVDV	
HCoV-NL63	..MK	LFLI	LLVLP	LASCFTCNNSNANLSMLQLGVDPNSSTIVTGLLPTHW.FCANQSTSV
HCoV-HKU1	....MLL	II	II	ILPTT.LAVIGDF.....NCTNF.....AIN..DLNTTVPRISEYVVVDV
	40	50	60	70
S-CryoEM	SFTR	GVYY	PDKVFRSS	VLHSTQDLFLPFFSNV...TWFHAIH
SARS-CoV-2	SFTR	GVYY	PDKVFRSS	VLHSTQDLFLPFFSNV...TWFHAIH
SARS-CoV	SSMR	GVYY	PDEIFRSD	TLYLTDLFLPFFSNV...TGFHTIN.....HT....
MERS-CoV	SKAD	GIIY	PQGRITYS	NIITYQGLF.PYQGDHGDYVYSAGHATGTTTPQKLFVANYSQD.
HCoV-229E	....			
HCoV-OC43	TNGL	GTYY	VLDREVLT	NTTLFNLGYYP
HCoV-NL63	YSAN	GF	FYIDVGNHRS	SAFALHTGY
HCoV-HKU1	SYGL	GTYY	IILDRVYL	NTTILFTGY
	80			
S-CryoEM	....			....
SARS-CoV-2	....			....
SARS-CoV	....			....
MERS-CoV	....			....
HCoV-229E	....			....
HCoV-OC43	....			....
HCoV-NL63	....			....
HCoV-HKU1	....			....
	90	100	110	
S-CryoEM	VLP	FND	GVYFAST.....	EK....SNIIRGWIF
SARS-CoV-2	VLP	FND	GVYFAST.....	EK....SNIIRGWIF
SARS-CoV	VIP	FKD	GIYFAAT.....	EK....SNVVRGWVF
MERS-CoV	VKQ	FAN	GFVVRIGA..AANSTG.....	TVIISP.STSATIRKIYPAFML
HCoV-229E	....			....
HCoV-OC43	LSD	F	IN	GI
HCoV-NL63	TFD	F	LS	NA
HCoV-HKU1	LSD	F	NN	GI
	120	130	140	
S-CryoEM	....			....
SARS-CoV-2	....			....
SARS-CoV	....			....
MERS-CoV	....			....
HCoV-229E	....			....
HCoV-OC43	....			....
HCoV-NL63	....			....
HCoV-HKU1	....			....
	150	160		
S-CryoEM	LG	VYYHKN.....		
SARS-CoV-2	LG	VYYHKN.....		
SARS-CoV	FAV	SKPMG.....		
MERS-CoV	SGNH	CPAGNSYTSFATYHTPATDCSDGNY.....		
HCoV-229E	SGGI	IPSDFAFNN.WFLLTNTSSVVDGVVRSFQPLLL		
HCoV-OC43	TSCH	PKLGNHFKELWHLDTIGVVSC.....		
HCoV-NL63	QDGR	IPNGFPFNN.WFLLTNGSTLVDGVSRLYQPLRL		
HCoV-HKU1	TICK	SK.GSSRNESWHFDKSEPLCL.....		
	170	180	190	200
S-CryoEM	....			....
SARS-CoV-2	....			....
SARS-CoV	....			....
MERS-CoV	....			....
HCoV-229E	....			....
HCoV-OC43	....			....
HCoV-NL63	....			....
HCoV-HKU1	....			....
	210	220	230	240
S-CryoEM	IN	LVRDLPQGFS	SALEPLVD	LPIGIN
SARS-CoV-2	IN	LVRDLPQGFS	SALEPLVD	LPIGIN
SARS-CoV	ID	VVRDLP	SGFNTLKP	IFKLPLGIN
MERS-CoV	....			....
HCoV-229E	....			....
HCoV-OC43	....			....
HCoV-NL63	....			....
HCoV-HKU1	....			....
	250			
S-CryoEM	....			....
SARS-CoV-2	....			....
SARS-CoV	....			....
MERS-CoV	....			....
HCoV-229E	....			....
HCoV-OC43	....			....
HCoV-NL63	....			....
HCoV-HKU1	....			....



	260	270	280	290		
S-CryoEM	.....G....DSSSGWTAGAAAYVGYLQPR	TFFLLKYNN	GTITD	AVDCAL		
SARS-CoV-2	.....G....DSSSGWTAGAAAYVGYLQPR	TFFLLKYNN	GTITD	AVDCAL		
SARS-CoV	.....PAQDIWGTSAAYFVGYLKPT	TFFMLKYDEN	GTITD	AVDCSQ		
MERS-CoV	.....Q....SDRKAW....AAFYVYKLQPL	TFFLLDFSV	DGYIRRA	AIDCGF		
HCoV-229E	TGHFYINGYRYFTLGNVEAVNFNVTTAETD	FTCTVALIASYADVLNVVSQTS	IANII	IYCN.		
HCoV-OC43	.....RRDIGFTLEYWVTPITSR	QYLLAFNQD	GIIFN	AVDCMS		
HCoV-NL63	TGQFYINGFKYFDLGFIEAVNFNVTTASATD	FWTVAFATFVDVLNVVSATN	IQN	LLYCD.		
HCoV-HKU1	.....SSNTDNETLQYWVTPITSKR	QYLLKFDNRC	GVITN	AVDCSS		
	300	310	320	330	340	350
S-CryoEM	DP	LSETKCTLK	SFTVEKGIYQTSNFRVQPTES	IVRFPNITNL	CPFGEVFN	NATRFASVYAW
SARS-CoV-2	DP	LSETKCTLK	SFTVEKGIYQTSNFRVQPTES	IVRFPNITNL	CPFGEVFN	NATRFASVYAW
SARS-CoV	NP	LAE	LKCSVK	SFEIDKGIYQTSNFRVQPTES	IVRFPNITNL	CPFGEVFNATKFPSSVYAW
MERS-CoV	ND	LSQLHCSYES	FDVESGVYSSVSSFEAKPSGSVVEQAEG	VECD	DFSPLLSG	.TPPQVYNF
HCoV-229E	SV	INRLRCDQLS	FDVDPDGFYSTSPIQSVLPVSIIVSLPV	.....	.....	.....Y
HCoV-OC43	DF	MEIKCKTQSI	APPTGVYELNGYTVQPIADVYRRKPDLPNCNIEAWL	NDKSVPS	PLNW	.....Y
HCoV-NL63	SP	FEKLQCEHLQ	FGGLQDGFYSANFLDDNVLPETTYVALPI	.....	.....	.....Y
HCoV-HKU1	SF	SEIQCKTKSL	LENTGVYDLSGFTVKEVATVHRRIPDLPDCDIDKWL	NNFNVPS	PLNW	.....Y
	360	370	380	390	400	
S-CryoEM	NRKRI	(SNC)VADYSVLYNSASFSTFKCYGVSPTKLNDLC	FTNV	.....YADSF	VIRGDEV	
SARS-CoV-2	NRKRI	(SNC)VADYSVLYNSASFSTFKCYGVSPTKLNDLC	FTNV	.....YADSF	VIRGDEV	
SARS-CoV	ERKKI	(SNC)VADYSVLYNSTFFSTFKCYGVSAATKLNLDLC	FSNV	.....YADSF	VVGDDV	
MERS-CoV	KRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAATIASN	CYSSL	.....ILDYFSYPLSMK	.....	.....	
HCoV-229E	HKHFTFIVLY	.....VDFKPSQSGGKCFNCYPAGVNITLANFNET	.....K	.....	.....	
HCoV-OC43	ERKTF	(SNC)NFMSSLSMSFIQADSFTCNNIDAAKIYGMCFSSI	.....TIDKFAIPNGRK	.....	.....	
HCoV-NL63	YQHTDINFT	.....ATASFSGSCYVCKPHQVNISLNG	.....N	.....	.....	
HCoV-HKU1	ERKIF	(SNC)NFNLSLTLRLVHTDSFSCNNFDESKIYGS	CFKSI	.....VLDKFAIPNSRR	.....	
	410	420	430	440	450	
S-CryoEM	RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGN	.....YNYLYRLFR	....	.....	.....	
SARS-CoV-2	RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGN	.....YNYLYRLFR	....	.....	.....	
SARS-CoV	RQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGN	.....YNYLYRLFR	....	.....	.....	
MERS-CoV	SDLSVSSAGPISQFNYSQSFNSPTCLILATVPHNLTITTKP	.....LKYSYINKC	....	.....	.....	
HCoV-229E	GPLCVDTSHEFTTKY	.....VAVYA	.....NVGRWSASINTGN	CPF..	.....	
HCoV-OC43	VDLQLGNLGYLQSSNYRIDTTATSCQLYYNLPAANVSVSFRNPSTWNKRF	(F)IEDSVFVP	.....	.....	.....	
HCoV-NL63	TSVCVR	(T)SHFSIRY	.....IYNRVKSGSPGDSSWHIYLKSGT	CPF..	.....	
HCoV-HKU1	SD	(L)QLGSSGFLQSSNYRIDTTSSSCQLYYSLPA(L)NVTINNYNPSSWNRRY	(F)GNNFN	....	.....	
	460	470	480			
S-CryoEM	.....KSNLKPFFERDI	.....STEIYQAGSTPCNGVEG	.....			
SARS-CoV-2	.....KSNLKPFFERDI	.....STEIYQAGSTPCNGVEG	.....			
SARS-CoV	.....HGKLRPFFERDI	.....SNVPFSPDGKPC(T)P.PA	.....			
MERS-CoV	.....SRLSSDDRTEV	.....PQLVNAVQSGSP(C)SVIP	.....			
HCoV-229E	..SFGK.VNNFVKFGSVCFSLKDIPGGC(A)M	.....PI	.....			
HCoV-OC43	QPTGVFTNHSVVYAQHCFAKPKNFCPC(K)L	..NGSCPGKNNIG(T)CPAGTNYLT(C)DNL(C)	.....			
HCoV-NL63	..SFSK.LNNFQKFKTICFSTVEVPSCNF	.....PL	.....			
HCoV-HKU1	.....LSSHVVYSRYCFSVNNFTCPCAK(P)SPASSCKSHKPPSA(S)CPIGTNYRS(C)ESTT.	.....	.....			
	490	500	510			
S-CryoEM	FNC	.....YF..PLQSYGFQP	.....TNGVGQ..PYRVVV	.....		
SARS-CoV-2	FNC	.....YF..PLQSYGFQP	.....TNGVGQ..PYRVVV	.....		
SARS-CoV	LNC	.....YF..PLQSYGFQP	.....TNGVGQ..PYRVVV	.....		
MERS-CoV	STVWEDGDYRKQLS	..PLEGGGWLV	.....ASGSTVA..MTEQLQ	.....		
HCoV-229E	VANWAYSYYT	.....	.....	.....		
HCoV-OC43	..TLDP(I)	.....TFKAPGTYKCPQTKSLVGIGEHCSGLAVKSDYCR	.....GNS	.....		
HCoV-NL63	EATWHYTSYTI	.....	.....	.....		
HCoV-HKU1	..VLDHTDWCRCSCLPDPITAYDPRSCSQKKS(L)VGVEHCA(G)FGVDEEKCGLDGSYNVS	.....	.....	.....		
	520	530	540			
S-CryoEM	.....LS	.....FELL...HAPATVCGP	....KKS(TN)LVKNK(CV)NF			
SARS-CoV-2	.....LS	.....FELL...HAPATVCGP	....KKS(TN)LVKNK(CV)NF			
SARS-CoV	.....LS	.....FELL...HAPATVCGP	....KKS(TN)LVKNK(CV)NF			
MERS-CoV	.....MG	.....FELL...HAPATVCGP	....KKS(TN)LVKNK(CV)NF			
HCoV-229E	...IGSLYVSWSDGDGITGVP	.....QPVE	.....GVSSFMN(V)TLDK(C)TKY			
HCoV-OC43	CTCQPAFLGWSADSLQGDKNIFANLILHDVNSGLT(C)ST	..DLQKANT(D)ILGV(CV)NY	.....			
HCoV-NL63	...VGALYVTWSEGNISITGVP	.....YPVS	.....GIREFSN(L)VLNN(C)TKY			
HCoV-HKU1	CLCSTDAFLGWSYDTCVSNRNCNIFSNFILNGINSGLT(C)SN	..DLLQPN(TE)VFTDV(CV)DY	.....			



	550	560	570	580	590	
S-CryoEM	NFNGLTGTGVLTESNKKFL.PFQQFGRD.IADTTD.AVRDPQTLLEILDITPCSFGGVSVI					
SARS-CoV-2	NFNGLTGTGVLTESNKKFL.PFQQFGRD.IADTTD.AVRDPQTLLEILDITPCSFGGVSVI					
SARS-CoV	NFNGLTGTGVLTSPSKRFQ.PFQQFGRD.VSDFTD.SVRDPKTSEILDITPCSFGGVSVI					
MERS-CoV	SLYGVSGRGVFNCTAVGV.RQQRFFVD.AYQNLVGYYSDD..DGNYYCLRACVSVPVSVI					
HCoV-229E	NIYDVSGGVGVIRVSNDFLNGI...TYTSTSGNLL.GFKDVTGKIYISITPCNPDLQLVV					
HCoV-OC43	DLYGISGQGIFFEVNATYYNSWQNLLYD.SNGNLY.GFRDYITNRTFMIRSCYSGRVSAA					
HCoV-NL63	NIYDVVGTGIIIRSSNQSLAGGI...TYVSNSGNLL.GFKNVSTGNIFIVTPCNQPDQVAV					
HCoV-HKU1	DLYGITGQGIFFKEVSAVYYNSWQNLLYD.SNGNII.GFKDFVTNKTYNIFPCYAGRVSAA					
	600	610	620	630	640	650
S-CryoEM	TPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT..PTWRVYSTGSNVFQTRAGCLIGA EHV					
SARS-CoV-2	TPGTNTSNQVAVLYQDVNCTEVPVAIHADQLT..PTWRVYSTGSNVFQTRAGCLIGA EHV					
SARS-CoV	TPGTNASSEVAVLYQDVNCTDVSTAIHADQLT..PAWRIYSTGNVVFQTRAGCLIGA EHV					
MERS-CoV	YD..KETKTHATLFGSVACEHISSTMSQYSRSTRSMLKRRDSTYGPLOTPVGCVLGLVNS					
HCoV-229E	YQ.....QAVVGAMLSNFSTSYGFSNVVEL.....PKFFYAS.....NGTYNC					
HCoV-OC43	FH..ANSSEPALLFRNLIKCNVFNNSLTRQLQ.....PINYSFDSYLGCVVNA YNS					
HCoV-NL63	YQ.....QSIIGAMTAVNESRYGLQNLQL.....PNFYVVS.....NGGNNC					
HCoV-HKU1	FH..QNASSLALLYRNLIKCSYVLNNISLT.....TQPYFDSYLGCVFNADNL					
	660	670	680	690	700	
S-CryoEM	N..NSYECDIPIGAGICASYQTQT.NSPA...SVAS.QSI...I.AYTM.SLGAENSV..A					
SARS-CoV-2	N..NSYECDIPIGAGICASYQTQT.NSPRRASVAS.QSI...I.AYTM.SLGAENSV..A					
SARS-CoV	D..TSYECDIPIGAGICASYHTVS.L...LRSTSQ.KSI...V.AYTM.SLGAADSSI..A					
MERS-CoV	S..LFVEDCKPLGQSLCALPDPSTLTTPRSVRSVPG.EMRLASI.AFNHPIQV.DQL.N					
HCoV-229E	TD...AVLTYSFGVCAAGSIIA...VQPRNV.....SY...DSV.SA					
HCoV-OC43	TAISVQTCDLTVGSGYCYVDYSK....NRRRSRAITTGYRFTNFEPFTVNS.VNDSLEPV					
HCoV-NL63	TT...AVMTYSNFGICADGSLIP....VRPRNS.....SD...NGI.SA					
HCoV-HKU1	TDYSVSSCALRMGSGFCVDYNSPSSSSSSRRKRSISASyRFVTfEPFNVSF.VNDSIESV					
	710	720	730	740	750	760
S-CryoEM	YSNNSIAIPTNFTISVTEILPVSMKTSTVDCTMYICGDSTECSNLLOQYGSFCTQLNRA					
SARS-CoV-2	YSNNSIAIPTNFTISVTEILPVSMKTSTVDCTMYICGDSTECSNLLOQYGSFCTQLNRA					
SARS-CoV	YSNNTIAIPTNFTISITTEVMPVSMKTSTVDCTMYICGDSTECANLLOQYGSFCTQLNRA					
MERS-CoV	SSYFKLSIPTNFTSFGVTQEIQTITQKVTVDCKQYVVCNGFQKCEQLLREYQGFCCKINQA					
HCoV-229E	IVTANLSPSNWTTTSVQVEYLQITSTPIVVDCTSTYVVCNGNVRCVELLKQYTSACKTIEDA					
HCoV-OC43	GGLYEIQIPSEFTIGNMEEFIQTSSTPKVTIDCAAFCVCGDYAACKLQVVEYGSFCDNINAI					
HCoV-NL63	IITANLSPSNWTTTSVQVEYLQITSTPIVVDCTATYVVCNGNPRCKNDLKQYTSACKTIEDA					
HCoV-HKU1	GGLYEIKIPTNFTIVGQEEFIQTNSPKVTIDCSLFCVCSNYAACCHDLISEYGTFCDNINSI					
	770	780	790	800	810	
S-CryoEM	LTGTAVEQDKNTQEVFAQVKQIYKTPPIKDFG....GF.NFSQILP.D...PSKPSKRS					
SARS-CoV-2	LTGTAVEQDKNTQEVFAQVKQIYKTPPIKDFG....GF.NFSQILP.D...PSKPSKRS					
SARS-CoV	LSGIAAEQDRNTREVFVAQVKQMYKTPTLKYFG....GF.NFSQILP.D...PLKPTKRS					
MERS-CoV	LHGANLRQDDSVRNLFASVKSQSSSPIIPGFG....GDFNLTLLEP.VSISTGSRARS					
HCoV-229E	LRNSARLESADVSEMLTFDKKAFTLANVSSF.....GDYNLSSVIPSLPTSGSRVAGRS					
HCoV-OC43	LTEVNELLDTTQLQVANSLMNGVTLSLKLKDGVNFNVDINFPVLGCLGSECSKASSRS					
HCoV-NL63	LRLSAHLETNDVSSMLTFDSNAFSLANVTSF.....GDYNLSSVLPQRNIRSSRIAGRS					
HCoV-HKU1	LDEVNGLLDTTQLHVADTLMQGVTLSSNLNTNLHFDVDNINFKSLVGCCLGPHCGS.SRS					
	820	830	840	850	860	870
S-CryoEM	FIEDLLFNKVTLADAGFIK.QYGDCL..GDIAARDLICAKFNGLTVLPPLLTDemiaQY					
SARS-CoV-2	FIEDLLFNKVTLADAGFIK.QYGDCL..GDIAARDLICAKFNGLTVLPPLLTDemiaQY					
SARS-CoV	FIEDLLFNKVTLADAGFMK.QYGDCL..GDINARDLICAKFNGLTVLPPLLTDDMIAAY					
MERS-CoV	AIEDLLFDKVTIADPGYMQ.GYDECMQO.GPASARDLICAQYVAGYKVLPLPLMDVNMEAAAY					
HCoV-229E	AIEDLLFSKLVTSGLGTVDADYKKCT..KGLSIADLACAOYNGIMVLPGVADAERMAMY					
HCoV-OC43	AIEDLLFDKVKLSDVGFVE.AYNNCT..GGAEIRDLCVQSYKGIKVLPLPLSENQISGY					
HCoV-NL63	ALEDLLFSKVVTSGLGTVDVGYKCT..KGLSIADLACAOYNGIMVLPGVADAERMAMY					
HCoV-HKU1	FFEDLLFDKVKLSDVGFVE.AYNNCT..GGSEIRDLCVQSFNGIKVLPLPILSESQISGY					
	880	890	900	910	920	930
S-CryoEM	TSALLAGTITSGWTFGAGAAQLQIPFAMQMA YRFNGIGVTONVLYENQKLIANQFN SAI GK					
SARS-CoV-2	TSALLAGTITSGWTFGAGAAQLQIPFAMQMA YRFNGIGVTONVLYENQKLIANQFN SAI GK					
SARS-CoV	TAALVSGTATAGWTFGAGAAQLQIPFAMQMA YRFNGIGVTONVLYENQKLIANQFN KAI SQ					
MERS-CoV	TSSLIGSIAGVGTAGLSSFAAIPFAQSIFYRLNGVGITQOVLSENQKLIANKFNQALGA					
HCoV-229E	TGSLIGGIAGLGLTSA...VSIPFSLAIQARLN YVALQTDVLOENQKLI AASFNKAMTN					
HCoV-OC43	TLAATSASLFPWPWTA...AGVPFFYLVNQYRINGLGVMTDVLSONQKLIANAFNNALYA					
HCoV-NL63	TGSLIGGMVLGGLTSA...AAIPFSLALQARLN YVALQTDVLOENQKLI AASFNKAINN					
HCoV-HKU1	TTAATVAAMFPWPWTA...AGIPFSLVNVQYRINGLGVMTDVLNKNQKLIATAFNNALLS					



	940	950	960	970		
S-CryoEM	IQDSLSSTA.....	SALGKLDVVNQNAQALNTLVKQLSSNFGAISSVLND				
SARS-CoV-2	IQDSLSSTA.....	SALGKLDVVNQNAQALNTLVKQLSSNFGAISSVLND				
SARS-CoV	IQESLTTTS.....	TALGKLDVVNQNAQALNTLVKQLSSNFGAISSVLND				
MERS-CoV	MQTGFTTTN.....	EAFRRKVVQDAVNNNAQALSKLASELSNTFGAISASIGD				
HCoV-229E	IVDAFTGVNDAITQTSQALQTVAT	TALNKIQDVVNQNGNSLNHLTSQLRQNFQAISSSIQA				
HCoV-OC43	IQQGFDAATN.....	SALVKIQAVVNANAEALNNLLQQLSNRFGAISASLQE				
HCoV-NL63	IVASFSSVNDAITQTAEAIHTVTI	TALNKIQDVVNQGSALNHLTSQLRHNFGAISNSIQA				
HCoV-HKU1	IQNGFSATN.....	SALAKIQSVVNSNAQALNSLLQQLFNKFGAISSSLQE				
	980	990	1000	1010	1020	1030
S-CryoEM	ILSRDLKVEAEVQIDRLITGRLOS	IQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKR				
SARS-CoV-2	ILSRDLKVEAEVQIDRLITGRLOS	IQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKR				
SARS-CoV	ILSRDLKVEAEVQIDRLITGRLOS	IQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKR				
MERS-CoV	IIQRDLVLEQDAQIDRLINGRLIT	LNAFVAQQLVRSESAALSAQLAKDKVNECVKASQSKR				
HCoV-229E	IYDRDLTIQADQQVDRILITGRIT	LNVFVSHLTLYTEVRASRQLAQKQVNECVKASQSKR				
HCoV-OC43	ILSRDLALEAEQIDRLINGRLIT	TALNAYVSQQLSDSTLVKFSAAQAMEKVNECVKSSSR				
HCoV-NL63	IYDRDLDSIQADQQVDRILITGRIT	LNAFVSVLNLKYTEVRGSRRLAQKKINECVKSSQNR				
HCoV-HKU1	ILSRDLALEAQVQIDRLINGRLIT	LNAYVSQQLSDISLVKFGAALAMEKVNECVKSSQSPR				
	1040	1050	1060	1070	1080	1090
S-CryoEM	VDFCCKGYHLMSPQSAPHGVVFHEVTYVPAQEKNFTTAPATICHDKGA...HF	PREGVVFV				
SARS-CoV-2	VDFCCKGYHLMSPQSAPHGVVFHEVTYVPAQEKNFTTAPATICHDKGA...HF	PREGVVFV				
SARS-CoV	VDFCCKGYHLMSPQAAPHGVVFHEVTYVPSQERNFTTAPATICHDKGA...YF	PREGVVFV				
MERS-CoV	SGFCCKGQTHIVSFVNNAPNGLYFMEHVGYYPSNHIEVVSAYGLCDAA	NPTNCIAPVNGYFI				
HCoV-229E	YGFCCNGTHIFSIIVNAAPGELVFHTVLLPTQYKDVEAWSGLCVDGTN..GYVLRQPNLA					
HCoV-OC43	INFCNGNHIISLVQNAPYGLYFHFNVVPTKYVTAKVSPGLCIAGNR..GIA	PKSGYFV				
HCoV-NL63	YGFCCNGTHIFSIIVNSAPDGLLFHTVLLPTDYKNVKAWSGICVDGIY..GYVLRQPNLV					
HCoV-HKU1	INFCNGNHIISLVQNAPYGLLFHMFYSYKPI	SFKTVLVSPGLCISGDV..GIA	PKQGYFI			
	1100	1110	1120	1130	1140	
S-CryoEM	SN.....GTHW	FVTRQNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQ..PELDSFK				
SARS-CoV-2	SN.....GTHW	FVTRQNFYEPQIITDNTFVSGNCDVVIGIVNNTVYDPLQ..PELDSFK				
SARS-CoV	FN.....GTSW	FITQRFSPQIITDNTFVSGNCDVVIGIVNNTVYDPLQ..PELDSFK				
MERS-CoV	KTNNTTRIVDEWSYTGSSFYAPEPIITSLN	TKYVAPQVTYQN..ISTNLPPPLLGNS	TGIDFQ			
HCoV-229E	LY...KEGNY	YRITSRIMFEPRIETMADFVQIENCNVT	FVNI	SRSEL..QTIV	PEYIDVN	
HCoV-OC43	NV.....NNTWMY	TGSGYYYPEPITENN	VVVMSTCAVNYTKAPYVML..NTS	PNLPDFK		
HCoV-NL63	LY...SDNGV	FRVTSRVMFQPRLPVLSDFVQIYNCNVT	FVNI	SRVEL..HTVI	PDYVDVN	
HCoV-HKU1	KH.....NDHW	MTGSSYYYPEPISDKNVVFMNTCSV	NFTKAPLVYL..NHSV	PKLSDFE		
	1150	1160	1170	1180	1190	
S-CryoEM	EELDKYFKNHST.PDVDLG.D	ISGINASVVNI.....	QKEIDRLNEVAKNL			
SARS-CoV-2	EELDKYFKNHST.PDVDLG.D	ISGINASVVNI.....	QKEIDRLNEVAKNL			
SARS-CoV	EELDKYFKNHST.PDVDLG.D	ISGINASVVNI.....	QKEIDRLNEVAKNL			
MERS-CoV	DELDEFKKNVST.SIPNFG.S	LTOINTTLDDL.....	TYEMLSLQQVVKAL			
HCoV-229E	KTLQELSYKLPN	YTVPLD..VVEQYNTILNL	TSEISTLENKSAELNYTVQK	LQTLIDNI		
HCoV-OC43	EELDQWFKNQTS.VAPDL	LSL..DYINVTFLDL.....	QVEMNRLQEA	AIKVL		
HCoV-NL63	KTLQEFANLPKYVKPNF..D	LTPENLTYLNL	LSSELKQLEAKTASLFQTTVE	LQLIDQI		
HCoV-HKU1	SELSHWFKNQTS.IAPNL	TLNLHTINATFLDL.....	YEMNLIQESIKSL			
	1200	1210	1220			
S-CryoEM	NESLIDLQELGKYEQYIKWP	SGRLVPRGSPGSGYIPEAP.....				
SARS-CoV-2	NESLIDLQELGKYEQYIKWP	WYIWLGFIA...GLIAIVMVTIML	CCMTSCCSCLK.....			
SARS-CoV	NESLIDLQELGKYEQYIKWP	WYIWLGFIA...GLIAIVMVTIML	CCMTSCCSCLK.....			
MERS-CoV	NESYIDLKELGNYTYNKP	WYIWLGFIA...GLVALALCVFFIL	CGTGCGTNCM.....			
HCoV-229E	NSTLVVDLKLNRVET	YIKWPWWVWLICISV...VLIFVVS	MLLCCSTGCGGFFSCFASS			
HCoV-OC43	NHSYINLKDIGTYEYVYKWP	WYIWLICL...AGVAMLVLLFFI	CCGTGCGTSCF.....			
HCoV-NL63	NSTYVDLKLNRFENYIKWP	WYIWLISV...VFVLLSLLVFC	CLSTGCGCCNCLTSS			
HCoV-HKU1	NNSYINLKDIGTYEYVYKWP	WYIWLISE...SFIIFLVLLFFI	CCGTGCGSACF.....			
	1230	1240	1250			
S-CryoEM	.....RDGQ..AYV.RK	DGEWVLLSTFLGHHHHHH				
SARS-CoV-2	..GCCSCGSCCKFD.ED	DSEPVLKGVKLHYT...				
SARS-CoV	..GACSCGSCCKFD.ED	DSEPVLKGVKLHYT...				
MERS-CoV	..GKLKCNRCDDRYEYD	LEPHKVHVH.....				
HCoV-229E	IRGCC..STKLPPYDVEK.....	IHIQ.....				
HCoV-OC43	..K..KGGCCDDYTGQ	ELVIKTHDD.....				
HCoV-NL63	MRGCCD..STKLPPYEF	EK.....VHVQ.....				
HCoV-HKU1	..S..KCHNCCDEYGGH	HD.FVIKTHDD.....				

## Movies Captions

**Movie S1:** Simulation of LA-bound SARS-CoV-2 S trimer colored in cyan, green and pink in the locked conformation, viewed from the side. LA is shown as spheres.

**Movie S2:** Simulation of SARS-CoV-2 S trimer in the locked form, close up view of LA-bound pocket. LA is shown as spheres. Amino acids interacting with the ligand are shown as sticks.

**Movie S3:** Simulation of SARS-CoV-2 S trimer colored in cyan, green and pink in the open form, viewed from the side. The RBD of one S monomer (colored in pink) adopts the ‘up’ position. LA is shown as spheres.

**Movie S4:** Animated structure of LA-bound SARS-CoV-2 S trimer colored in cyan, green and pink. Morphing of apo S (PDBID 6VXX (7)) to LA-bound S is illustrated.

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